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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=12; min=45; sec=12; ms=146;]

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Reviewer Comments:

Leu Glu Phe
30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile
35 40 45

Please correct invalid amino acid numbering shown above in sequence id# 48. Please check the remaining sequences for similar errors.

Application No: 10785116 Version No: 3.0

Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
Finished: 2009-01-07 15:10:52.884
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 492 ms
Total Warnings: 33
Total Errors: 9
No. of SeqIDs Defined: 49
Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (24)
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Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
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Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (36)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (41)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (45)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (46)

SEQUENCE LISTING

<110> Pecker, Iris

Vlodavsky , Israel

Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 27674

<140> 10785116

<141> 2004-02-25

<160> 49

<170> PatentIn version 3.1

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<212> DNA

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gtagtgtatgc catgttaactg aatc

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<210> 4

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

<400> 4

gcatcttagc cgtctttctt cg

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<211> 24

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<213> Artificial sequence

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<223> Synthetic oligonucleotide

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<210> 8

<211> 9

<212> PRT

<213> Artificial sequence

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1 5

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<211> 543
<212> PRT
<213> Homo sapiens

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35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Gly Ser Pro Lys Leu
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
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Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
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Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
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Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
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Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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<211> 1721
<212> DNA
<213> Homo sapiens

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<222> (63) .. (1691)
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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu

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Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu				
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aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag			299	
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys				
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Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly				
80	85	90	95	
ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc			395	
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr				
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Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys				
115	120	125		
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Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu				
130	135	140		
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Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys				
145	150	155		
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Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr				
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Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu				
180	185	190		
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc			683	
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu				
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Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly				
210	215	220		
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Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly				
225	230	235		

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tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro 260 265 270	875
cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly 275 280 285	923
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